

SEQUENCE LISTING

<110> Lanahan, Michael
Miller, Edward S.
Kelly, Robert M.

<120> METHODS FOR HIGH-TEMPERATURE HYDROLYSIS OF GALACTOSE-CONTAINING OLIGOSACCHARIDES IN COMPLEX MIXTURES

<130> 9207.4

<150> US 60/220,211

<151> 2000-07-22

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1659

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1659)

<223>

<400> 1

atg gaa ata ttc gga aag acc ttc aga gag gga aga ttc gtt ctc aaa
Met Glu Ile Phe Gly Lys Thr Phe Arg Glu Gly Arg Phe Val Leu Lys
1 5 10 15

48

gag aaa aac ttc aca gtt gag ttc gcg gtg gag aag ata cac ctt ggc
Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly
20 25 30

96

tgg aag atc tcc ggc agg gtg aag gga agt ccg gga agg ctt gag gtt
Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val
35 40 45

144

ctt cga acg aaa gca ccg gaa aag gta ctt gtg aac aac tgg cag tcc
Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser
50 55 60

192

tgg gga ccg tgc agg gtg gtc gat gcc ttt tct ttc aaa cca cct gaa
Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu
65 70 75 80

240

ata gat ccg aac tgg aga tac acc gct tcg gtg ccc gat gta ctt
Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu
85 90 95

288

gaa agg aac ctc cag agc gac tat ttc gtg gct gaa gaa gga aaa gtg Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val 100 105 110	336
tac ggt ttt ctg agt tcg aaa atc gca cat cct ttc ttc gct gtg gaa Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe Ala Val Glu 115 120 125	384
gat ggg gaa ctt gtg gca tac ctc gaa tat ttc gat gtc gag ttc gac Asp Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val Glu Phe Asp 130 135 140	432
gac ttt gtt cct ctt gaa cct ctc gtt gta ctc gag gat ccc aac aca Asp Phe Val Pro Leu Glu Pro Leu Val Val Leu Glu Asp Pro Asn Thr 145 150 155 160	480
ccc ctt ctt ctg gag aaa tac gcg gaa ctc gtc gga atg gaa aac aac Pro Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Met Glu Asn Asn 165 170 175	528
gcg aga gtt cca aaa cac aca ccc act gga tgg tgc agc tgg tac cat Ala Arg Val Pro Lys His Thr Pro Thr Gly Trp Cys Ser Trp Tyr His 180 185 190	576
tac ttc ctt gat ctc acc tgg gaa gag acc ctc aag aac ctg aag ctc Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn Leu Lys Leu 195 200 205	624
gcg aag aat ttc ccg ttc gag gtc ttc cag ata gac gac gcc tac gaa Ala Lys Asn Phe Pro Phe Glu Val Phe Gln Ile Asp Asp Ala Tyr Glu 210 215 220	672
aag gac ata ggt gac tgg ctc gtg aca aga gga gac ttt cca tcg gtg Lys Asp Ile Gly Asp Trp Leu Val Thr Arg Gly Asp Phe Pro Ser Val 225 230 235 240	720
gaa gag atg gca aaa gtt ata gcg gaa aac ggt ttc atc ccc ggc ata Glu Glu Met Ala Lys Val Ile Ala Glu Asn Gly Phe Ile Pro Gly Ile 245 250 255	768
tgg acc gcc ccg ttc agt gtt tct gaa acc tcg gat gta ttc aac gaa Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val Phe Asn Glu 260 265 270	816
cat ccg gac tgg gta gtg aag gaa aac gga gag ccg aag atg gct tac His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr 275 280 285	864
aga aac tgg aac aaa aag ata tac gcc ctc gat ctt tcg aaa gat gag Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu 290 295 300	912
gtt ctg aac tgg ctt ttc gat ctc ttc tca tct ctg aga aag atg ggc Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly 305 310 315 320	960
tac agg tac ttc aag atc gac ttt ctc ttc gcg ggt gcc gtt cca gga Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly 325 330 335	1008

gaa aga aaa aag aac ata aca cca att cag gcg ttc aga aaa ggg att Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile 340 345 350	1056
gag acg atc aga aaa gcg gtg gga gaa gat tct ttc atc ctc gga tgc Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys 355 360 365	1104
ggc tct ccc ctt ctt ccc gca gtg gga tgc gtc gac ggg atg agg ata Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile 370 375 380	1152
gga cct gac act gcg ccg ttc tgg gga gaa cat ata gaa gac aac gga Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly 385 390 395 400	1200
gct ccc gct gca aga tgg gcg ctg aga aac gcc ata acg agg tac ttc Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe 405 410 415	1248
atg cac gac agg ttc tgg ctg aac gac ccc gac tgt ctg ata ctg aga Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg 420 425 430	1296
gag gag aaa acg gat ctc aca cag aag gaa aag gag ctc tac tcg tac Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr 435 440 445	1344
acg tgt gga gtg ctc gac aac atg atc ata gaa agc gat gat ctc tcg Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser 450 455 460	1392
ctc gtc aga gat cat gga aaa aag gtt ctg aaa gaa acg ctc gaa ctc Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu 465 470 475 480	1440
ctc ggt gga aga cca cgg gtt caa aac atc atg tcg gag gat ctg aga Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg 485 490 495	1488
tac gag atc gtc tct ggc act ctc tca gga aac gtc aag atc gtg Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val 500 505 510	1536
gtc gat ctg aac agc aga gag tac cac ctg gaa aaa gaa gga aag tcc Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser 515 520 525	1584
tcc ctg aaa aaa aga gtc gtc aaa aga gaa gac gga aga aac ttc tac Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr 530 535 540	1632
ttc tac gaa gag ggt gag aga gaa tga Phe Tyr Glu Glu Gly Glu Arg Glu 545 550	1659

<210> 2
<211> 552
<212> PRT
<213> Thermotoga maritime

<400> 2

Met Glu Ile Phe Gly Lys Thr Phe Arg Glu Gly Arg Phe Val Leu Lys
1 5 10 15

Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly
20 25 30

Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val
35 40 45

Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser
50 55 60

Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu
65 70 75 80

Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu
85 90 95

Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val
100 105 110

Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe Ala Val Glu
115 120 125

Asp Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val Glu Phe Asp
130 135 140

Asp Phe Val Pro Leu Glu Pro Leu Val Val Leu Glu Asp Pro Asn Thr
145 150 155 160

Pro Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Met Glu Asn Asn
165 170 175

Ala Arg Val Pro Lys His Thr Pro Thr Gly Trp Cys Ser Trp Tyr His
180 185 190

Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn Leu Lys Leu
195 200 205

Ala Lys Asn Phe Pro Phe Glu Val Phe Gln Ile Asp Asp Ala Tyr Glu
210 215 220

Lys Asp Ile Gly Asp Trp Leu Val Thr Arg Gly Asp Phe Pro Ser Val
225 230 235 240

Glu Glu Met Ala Lys Val Ile Ala Glu Asn Gly Phe Ile Pro Gly Ile
245 250 255

Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val Phe Asn Glu
260 265 270

His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr
275 280 285

Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu
290 295 300

Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly
305 310 315 320

Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly
325 330 335

Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile
340 345 350

Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys
355 360 365

Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile
370 375 380

Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
385 390 395 400

Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
405 410 415

Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
420 425 430

Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
435 440 445

Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
450 455 460

Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu
465 470 475 480

Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
485 490 495

Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
500 505 510

Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
515 520 525

Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
530 535 540

Phe Tyr Glu Glu Gly Glu Arg Glu
545 550